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<110> Human Genome Sciences, Inc.

<120> Albumin Fusion Proteins

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<140> Unassigned

<141> 2001-04-12

<150> 60/229,358

<151> 2000-04-12

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<151> 2000-12-21

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<151> 2000-04-25

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<170> PatentIn Ver. 2.1

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Ile Ser Ala Asp Ala His Lys Ser
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Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg		480	
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
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tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc		528	
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
165	170	175	
tgc ctg ttg cca aag ctc gat gaa ctt cg gat gaa ggg aag gct tcg		576	
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
180	185	190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa		624	
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
195	200	205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc		672	
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
210	215	220	
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Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
225	230	235	240
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac		768	
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
245	250	255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc		816	
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
260	265	270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac		864	
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
275	280	285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca		912	
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
290	295	300	
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct		960	
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
305	310	315	320
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga		1008	
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg			
325	330	335	
agg cat cct gat tac tct gtc gtg ctg ctg aga ctt gcc aag aca		1056	
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr			
340	345	350	

tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa		1104	
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu			
355	360	365	
tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct		1152	
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro			
370	375	380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag		1200	
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu			
385	390	395	400
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc		1248	
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro			
405	410	415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa		1296	
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys			
420	425	430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt		1344	
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys			
435	440	445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat		1392	
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His			
450	455	460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc		1440	
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser			
465	470	475	480
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca		1488	
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr			
485	490	495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat		1536	
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp			
500	505	510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca		1584	
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala			
515	520	525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg		1632	
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu			
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aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag		1680	
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Glu	Thr	Cys	Phe
565			Ala
		Glu	Gly
		Lys	Lys
		Leu	Val
		570	575
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		10	Glu
			15
Glu	Asn	Phe	Lys
Ala	Leu	Val	Leu
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		Phe	Gln
		Ala	Tyr
		Gln	Leu
		30	
Gln	Cys	Pro	Phe
Glu	Asp	His	Val
35		Lys	Leu
		Val	Asn
		Glu	Val
		40	Thr
			Glu
Phe	Ala	Lys	Thr
Cys	Val	Ala	Asp
50		Glu	Ser
		Asn	Ala
		Cys	Cys
		55	Asp
			Lys
Ser	Leu	His	Thr
Leu	Phe	Gly	Asp
65		Lys	Leu
		Cys	Thr
		75	Val
			Ala
			Thr
			Leu
Arg	Glu	Thr	Tyr
Gly	Glu	Met	Ala
85		Asp	Asp
		Cys	Cys
		90	Ala
			Lys
			Gln
			Glu
			Pro
Glu	Arg	Asn	Glu
Cys	Phe	Leu	Gln
100		His	Lys
		Asp	Asp
		Asn	Asn
		105	Leu
Pro	Arg	Leu	Val
Arg	Pro	Glu	Val
115		Asp	Val
		Met	Cys
		120	Thr
			Ala
			Phe
			His
		125	
Asp	Asn	Glu	Glu
Thr	Phe	Leu	Lys
130		Tyr	Leu
		Glu	Tyr
		Ile	Ile
		140	Arg
Arg	His	Pro	Tyr
Tyr	Ala	Pro	Phe
145		Glu	Tyr
		Leu	Ala
		150	Lys
			Arg
Tyr	Lys	Ala	Ala
Phe	Thr	Glu	Cys
165		Cys	Gln
		Ala	Ala
		170	Asp
			Lys
			Ala
Cys	Leu	Leu	Pro
Lys	Leu	Asp	Glu
			Arg
			Asp
			Glu
			Gly
			Lys
			Ala
			Ser

180	185	190
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu		
195	200	205
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro		
210	215	220
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys		
225	230	240
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp		
245	250	255
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser		
260	265	270
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His		
275	280	285
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser		
290	295	300
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala		
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Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg		
325	330	335
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr		
340	345	350
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu		
355	360	365
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro		
370	375	380
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu		
385	390	400
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro		
405	410	415
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys		
420	425	430
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys		
435	440	445
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His		

450	455	460
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser		
465	470	475
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr		
485	490	495
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp		
500	505	510
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala		
515	520	525
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu		
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Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys		
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32

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<223> reverse primer useful for generation of albumin
fusion protein in which the albumin moiety is c-terminal of
the Therapeutic Protein

<220>
<221> misc_feature
<222> (38)
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<220>
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<223> n equals a,t,g, or c

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<222> (41)
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<220>
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<220>
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<223> n equals a,t,g, or c

<220>
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<222> (51)
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<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (52)
<223> n equals a,t,g, or c

<400> 28
ctttaaatcg atgagcaacc tcactttgt gtgcacnnnnnnnnnn nn      52

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> signal peptide of natural human serum albumin protein

<400> 29
Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
 1           5           10          15

Tyr Ser Arg Ser Leu Asp Lys Arg
 20

<210> 30
<211> 114
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of PC4:HSA
albumin fusion VECTOR

<220>
<221> misc_feature
<222> (5)..(10)
<223> BamHI restriction site

<220>
<221> misc_feature
<222> (11)..(16)
<223> Hind III restriction site

<220>
<221> misc_feature
<222> (17)..(27)
<223> Kozak sequence

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<220>
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<222> (25)..(97)
<223> cds natural signal sequence of human serum albumin

<220>
<221> misc_feature
<222> (75)..(81)
<223> XhoI restriction site

<220>
<221> misc_feature
<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

<400> 30
tcagggatcc aagcttccgc caccatgaag tggtaacct ttattccct tcctttctc 60
tttagctcggttactcgag gggtgtgttt cgatcgatg cacacaagag tgag           114

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
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<222> (6)..(11)
<223> Asp718 restriction site

<220>
<221> misc_feature
<222> (12)..(17)
<223> EcoRI restriction site

<220>
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<222> (15)..(17)
<223> reverse complement of stop codon

<220>
<221> misc_feature
<222> (18)..(25)
<223> AscI restriction site

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<220>
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<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

<400> 31
gcagcggtag cgaattcggc gcgcctata agcctaaggc agc 43

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

<220>
<221> misc_feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
<222> (30)
<223> n equals a,t,g, or c

<220>
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<220>
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<223> n equals a,t,g, or c

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<222> (33)
<223> n equals a,t,g, or c

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<221> misc_feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
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<220>
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<220>
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<222> (42)
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<222> (43)
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<220>
<221> misc_feature
<222> (44)
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<220>
<221> misc_feature
<222> (45)
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<223> n equals a,t,g, or c

<220>

<221> misc_feature

<222> (46)

<223> n equals a,t,g, or c

<400> 32
ccggcgctcg aggggtgtgt ttcgtcgann nnnnnnnnnn nnnnnn 46

<210> 33

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<223> reverse primer useful for inserting Therapeutic protein into pC4:HSA vector

<220>

<221> misc_feature

<222> (38)

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<220>

<221> misc_feature

<222> (39)

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<220>

<221> misc_feature

<222> (40)

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<223> n equals a,t,g, or c

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<222> (50)
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<222> (52)
<223> n equals a,t,g, or c

<220>
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<222> (53)
<223> n equals a,t,g, or c

<220>
<221> misc_feature
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<222> (54)
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<220>
<221> misc_feature
<222> (55)
<223> n equals a,t,g, or c

<400> 33
agtcccatcg atgagcaacc tcactttgt gtgcacnnnn nnnnnnnnnn nnnnn      55

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser
    1           5           10          15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Ala Leu
    1           5           10          15

Trp Ala Pro Ala Arg Gly
    20

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> Degenerate VH forward primer useful for
amplifying human VH domains

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<400> 36
caggtgcagc tggcagtc tgg 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 37
caggtaact taaggagtc tgg 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 38
gaggtgcagc tggcagtc tgg 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate VH forward primer useful for amplifying human VH domains

<400> 39
caggtgcagc tgcaggagtc ggg 23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<221>primer_bind
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<400> 40
gaggtgcagc tgttgcagtc tgc 23

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 41
caggtacagc tgcagcagtc agg 23

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 42
tgaggagacg gtgaccaggg tgcc 24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate JH reverse primer useful for amplifying human VH domains

<400> 43
tgaagagacg gtgaccattg tccc 24

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
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amplifying human VH domains

<400> 44
tgaggagacg gtgaccaggg ttcc                                24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate JH reverse primer useful for
amplifying human VH domains

<400> 45
tgaggagacg gtgaccgtgg tccc                                24

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 46
gacatccaga tgacctcagtc tcc                                23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 47
gatgttgtga tgactcagtc tcc                                23

<210> 48
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<212> DNA

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<213> Artificial Sequence	
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<223>Degenerate Vkappa forward primer useful for amplifying human VL domains	
<400> 48	
gatattgtga tgactcagtc tcc	23
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<211> 23	
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gaaatttgt tgacgcagtc tcc	23
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<211> 23	
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<400> 50	
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<211> 23	
<212> DNA	
<213> Artificial Sequence	
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<210> 52	
<211> 23	

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<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Vkappa forward primer useful for
amplifying human VL domains

<400> 52
gaaattgtgc tgactcagtc tcc 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 53
cagtctgtgt tgacgcagcc gcc 23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
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<400> 54
cagtctgccc tgactcagcc tgc 23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 55
tcctatgtgc tgactcagcc acc 23

<210> 56

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<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
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amplifying human VL domains

<400> 56
tcttctgagc tgactcagga ccc                                23

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
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amplifying human VL domains

<400> 57
cacgttatac tgactcaacc gcc                                23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate Vlambda forward primer useful for
amplifying human VL domains

<400> 58
caggctgtgc tcactcagcc gtc                                23

<210> 59
<211> 23
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amplifying human VL domains

<400> 59
aattttatgc tgactcagcc cca                                23

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<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 60
acgttgatt tccacccttgg tccc 24

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 61
acgttgatc tccagcttgg tccc 24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 62
acgttgata tccactttgg tccc 24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 63
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<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221>primer_bind
<223>Degenerate Jkappa reverse primer useful for
amplifying human VL domains

<400> 64
acgtttaatc tccagtcgtg tccc 24

<210> 65
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 65
cagtctgtgt tgacgcagcc gcc 23

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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amplifying human VL domains

<400> 66
cagtctgccc tgactcagcc tgc 23

<210> 67
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<223>Degenerate Jlambda reverse primer useful for
amplifying human VL domains

<400> 67

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tcctatgtgc tgactcagcc acc	23
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<211> 23	
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<400> 68	
tcttctgagc tgactcagga ccc	23
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<211> 23	
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<400> 69	
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<210> 70	
<211> 23	
<212> DNA	
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<400> 70	
caggctgtgc tcactcagcc gtc	23
<210> 71	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
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<223>Degenerate Jlambda reverse primer useful for amplifying human VL domains	

<400> 71
 aattttatgc tgactcagcc cca

 <210> 72
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221>turn
 <223>Linker peptide that may be used to join VH
 and VL domains in an scFv.

 <400> 72
 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

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 <210> 73
 <211> 23
 <212> PRT
 <213> Homo sapiens

 <400> 73
 Cys Cys Cys Ala Ala Gly Ala Ala Thr Thr Cys Cys Cys Thr Thr Ala
 1 5 10 15

 Thr Cys Cys Ala Gly Gly Cys
 20

 <210> 74
 <211> 429
 <212> PRT
 <213> Homo sapiens

 <400> 74
 Met Cys Pro Gly Ala Leu Trp Val Ala Leu Pro Leu Leu Ser Leu Leu
 1 5 10 15

 Ala Gly Ser Leu Gln Gly Lys Pro Leu Gln Ser Trp Gly Arg Gly Ser
 20 25 30

 Ala Gly Gly Asn Ala His Ser Pro Leu Gly Val Pro Gly Gly Leu
 35 40 45

 Pro Glu His Thr Phe Asn Leu Lys Met Phe Leu Glu Asn Val Lys Val
 50 55 60

 Asp Phe Leu Arg Ser Leu Asn Leu Ser Gly Val Pro Ser Gln Asp Lys
 65 70 75 80

 Thr Arg Val Glu Pro Pro Gln Tyr Met Ile Asp Leu Tyr Asn Arg Tyr

85	90	95
Thr Ser Asp Lys Ser Thr Thr Pro Ala Ser Asn Ile Val Arg Ser Phe		
100	105	110
Ser Met Glu Asp Ala Ile Ser Ile Thr Ala Thr Glu Asp Phe Pro Phe		
115	120	125
Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg His Glu Gln		
130	135	140
Ile Thr Arg Ala Glu Leu Arg Leu Tyr Val Ser Cys Gln Asn His Val		
145	150	155
Asp Pro Ser His Asp Leu Lys Gly Ser Val Val Ile Tyr Asp Val Leu		
165	170	175
Asp Gly Thr Asp Ala Trp Asp Ser Ala Thr Glu Thr Lys Thr Phe Leu		
180	185	190
Val Ser Gln Asp Ile Gln Asp Glu Gly Trp Glu Thr Leu Glu Val Ser		
195	200	205
Ser Ala Val Lys Arg Trp Val Arg Ser Asp Ser Thr Lys Ser Lys Asn		
210	215	220
Lys Leu Glu Val Thr Val Glu Ser His Arg Lys Gly Cys Asp Thr Leu		
225	230	240
Asp Ile Ser Val Pro Pro Gly Ser Arg Asn Leu Pro Phe Phe Val Val		
245	250	255
Phe Ser Asn Asp His Ser Ser Gly Thr Lys Glu Thr Arg Leu Glu Leu		
260	265	270
Arg Glu Met Ile Ser His Glu Gln Glu Ser Val Leu Lys Lys Leu Ser		
275	280	285
Lys Asp Gly Ser Thr Glu Ala Gly Glu Ser Ser His Glu Glu Asp Thr		
290	295	300
Asp Gly His Val Ala Ala Gly Ser Thr Leu Ala Arg Arg Lys Arg Ser		
305	310	320
Ala Gly Ala Gly Ser His Cys Gln Lys Thr Ser Leu Arg Val Asn Phe		
325	330	335
Glu Asp Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Glu Tyr Glu		
340	345	350
Ala Tyr Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Ala Asp Asp Val		

355	360	365	
Thr Pro Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Lys Phe			
370	375	380	
Pro Thr Lys Val Gly Lys Ala Cys Cys Val Pro Thr Lys Leu Ser Pro			
385	390	395	400
Ile Ser Val Leu Tyr Lys Asp Asp Met Gly Val Pro Thr Leu Lys Tyr			
405	410	415	
His Tyr Glu Gly Met Ser Val Ala Glu Cys Gly Cys Arg			
420	425		
<210> 75			
<211> 280			
<212> PRT			
<213> Homo sapiens			
<400> 75			
Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val Leu			
1	5	10	15
Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn Val Arg			
20	25	30	
Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly Asp Trp Met			
35	40	45	
Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln Asn Leu Gln Pro			
50	55	60	
Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp Leu Glu Val Asn Ile			
65	70	75	80
Ala Lys Val Asp Val Thr Glu Gln Pro Gly Leu Ser Gly Arg Phe Ile			
85	90	95	
Ile Thr Ala Leu Pro Thr Ile Tyr His Cys Lys Asp Gly Glu Phe Arg			
100	105	110	
Arg Tyr Gln Gly Pro Arg Thr Lys Lys Asp Phe Ile Asn Phe Ile Ser			
115	120	125	
Asp Lys Glu Trp Lys Ser Ile Glu Pro Val Ser Ser Trp Phe Gly Pro			
130	135	140	
Gly Ser Val Leu Met Ser Ser Met Ser Ala Leu Phe Gln Leu Ser Met			
145	150	155	160
Trp Ile Arg Thr Cys His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro			

165	170	175
Val Trp Gly Ser Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly		
180	185	190
Leu Leu Leu Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro		
195	200	205
Ser Lys Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu		
210	215	220
Leu Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu		
225	230	235
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu Gly		
245	250	255
Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser Leu Gly		
260	265	270
Pro Ser Leu Ala Thr Asp Lys Ser		
275	280	
<210> 76		
<211> 112		
<212> PRT		
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<400> 76		
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1	5	10
		15
Phe Arg Leu Pro Arg Lys Trp Gly Trp Arg Thr Glu Ala Thr Ala Pro		
20	25	30
His Ala Pro Val Pro Gln Ser Ile Cys Pro Arg Tyr Thr Ser Pro Cys		
35	40	45
Ala Pro His Asp Cys Gly Ser Gln Thr Val Gln Gly Asn Ser Leu Ser		
50	55	60
Leu Phe Tyr Thr Leu Ser His Lys Ala Pro Gln Leu Pro His Arg Val		
65	70	75
		80
Pro Ala Pro Leu Phe Cys Lys Tyr Val Lys Arg Lys Lys Cys Lys Arg		
85	90	95
Trp Ser Leu Gly Trp Ser Ser Ser Leu Gln Leu Arg Leu Leu Thr Met		
100	105	110
<210> 77		

<211> 346
<212> PRT
<213> Homo sapiens

<400> 77

Met	Asp	Pro	Ala	Arg	Lys	Ala	Gly	Ala	Gln	Ala	Met	Ile	Trp	Thr	Ala
1					5				10					15	
Gly	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Gly	Gly	Ala	Gln	Ala	Leu	Glu
		20						25						30	
Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	Gly	Cys	Ser	Pro	Asn	Lys
		35					40					45			
Met	Lys	Thr	Val	Lys	Cys	Ala	Pro	Gly	Val	Asp	Val	Cys	Thr	Glu	Ala
		50				55					60				
Val	Gly	Ala	Val	Glu	Thr	Ile	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Arg
		65			70				75					80	
Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn	Asp	Arg	Gly	Leu	Asp	Leu
		85				90						95			
His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu	Gln	Gln	Cys	Ala	Gln	Asp	Arg
		100				105						110			
Cys	Asn	Ala	Lys	Leu	Asn	Leu	Thr	Ser	Arg	Ala	Leu	Asp	Pro	Ala	Gly
		115				120					125				
Asn	Glu	Ser	Ala	Tyr	Pro	Pro	Asn	Gly	Val	Glu	Cys	Tyr	Ser	Cys	Val
		130				135				140					
Gly	Leu	Ser	Arg	Glu	Ala	Cys	Gln	Gly	Thr	Ser	Pro	Pro	Val	Val	Ser
		145			150				155				160		
Cys	Tyr	Asn	Ala	Ser	Asp	His	Val	Tyr	Lys	Gly	Cys	Phe	Asp	Gly	Asn
		165				170					175				
Val	Thr	Leu	Thr	Ala	Ala	Asn	Val	Thr	Val	Ser	Leu	Pro	Val	Arg	Gly
		180				185					190				
Cys	Val	Gln	Asp	Glu	Phe	Cys	Thr	Arg	Asp	Gly	Val	Thr	Gly	Pro	Gly
		195				200					205				
Phe	Thr	Leu	Ser	Gly	Ser	Cys	Cys	Gln	Gly	Ser	Arg	Cys	Asn	Ser	Asp
		210				215					220				
Leu	Arg	Asn	Lys	Thr	Tyr	Phe	Ser	Pro	Arg	Ile	Pro	Pro	Leu	Val	Arg
		225			230				235				240		
Leu	Pro	Pro	Pro	Glu	Pro	Thr	Thr	Val	Ala	Ser	Thr	Thr	Ser	Val	Thr

245	250	255
Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met		
260	265	270
Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala		
275	280	285
Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln		
290	295	300
Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln		
305	310	315
Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu		
325	330	335
Leu Leu Ala Val Ala Ala Gly Val Leu Leu		
340	345	
<210> 78		
<211> 272		
<212> PRT		
<213> Homo sapiens		
<400> 78		
Met Lys Gly Lys Lys Gly Ile Val Ala Ala Ser Gly Ser Glu Thr Glu		
1	5	10
15		
Asp Glu Asp Ser Met Asp Ile Pro Leu Asp Leu Ser Ser Ser Ala Gly		
20	25	30
Ser Gly Lys Arg Arg Arg Arg Gly Asn Leu Pro Lys Glu Ser Val Gln		
35	40	45
Ile Leu Arg Asp Trp Leu Tyr Glu His Arg Tyr Asn Ala Tyr Pro Ser		
50	55	60
Glu Gln Glu Lys Ala Leu Leu Ser Gln Gln Thr His Leu Ser Thr Leu		
65	70	75
80		
Gln Val Cys Asn Trp Phe Ile Asn Ala Arg Arg Arg Leu Leu Pro Asp		
85	90	95
Met Leu Arg Lys Asp Gly Lys Asp Pro Asn Gln Phe Thr Ile Ser Arg		
100	105	110
Arg Gly Ala Lys Ile Ser Glu Thr Ser Ser Val Glu Ser Val Met Gly		
115	120	125
Ile Lys Asn Phe Met Pro Ala Leu Glu Glu Thr Pro Phe His Ser Cys		

130	135	140
Thr Ala Gly Pro Asn Pro Thr Leu Gly Arg Pro Leu Ser Pro Lys Pro		
145	150	155
Ser Ser Pro Gly Ser Val Leu Ala Arg Pro Ser Val Ile Cys His Thr		
165	170	175
Thr Val Thr Ala Leu Lys Asp Val Pro Phe Ser Leu Cys Gln Ser Val		
180	185	190
Gly Val Gly Gln Asn Thr Asp Ile Gln Gln Ile Ala Ala Lys Asn Phe		
195	200	205
Thr Asp Thr Ser Leu Met Tyr Pro Glu Asp Thr Cys Lys Ser Gly Pro		
210	215	220
Ser Thr Asn Thr Gln Ser Gly Leu Phe Asn Thr Pro Pro Pro Thr Pro		
225	230	235
Pro Asp Leu Asn Gln Asp Phe Ser Gly Phe Gln Leu Leu Val Asp Val		
245	250	255
Ala Leu Lys Arg Ala Ala Glu Met Glu Leu Gln Ala Lys Leu Thr Ala		
260	265	270
<210> 79		
<211> 167		
<212> PRT		
<213> Homo sapiens		
<400> 79		
Met Leu Thr Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Ala Ser Gly		
1	5	10
15		
Asn Ala Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly		
20	25	30
Gly Gly Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro		
35	40	45
Ile Thr Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu		
50	55	60
Gln Val Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn		
65	70	75
80		
Gly Asp Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln		
85	90	95
Val Ser Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr		

100	105	110
Asp Lys Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe		
115	120	125
Asn Ala Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly		
130	135	140
Arg Ser Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr		
145	150	155
Pro Thr Ser Cys Ser Arg Cys		
165		

<210> 80
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals stop translation

<400> 80

Met Leu Ala Ala Leu Ala Cys Ser Trp Arg Leu Leu Ser Leu Gly Ala			
1	5	10	15

His Ser Gly Arg Ala Xaa			
20			

<210> 81
<211> 733
<212> DNA
<213> Homo sapiens

<400> 81			
gggatccgga gcccataatct tctgacaaaaa ctcacacatg cccaccgtgc ccagcacctg			60
aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga			120
tctcccgac tcctgaggc acatgcgtgg tggtgacgt aagccacgaa gaccctgagg			180
tcaagttcaa ctggtagtgc gacggcgtgg aggtgcataaa tgccaagaca aagccgcggg			240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact			300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccacatcg			360

agaaaaccat	ctccaaagcc	aaagggcagc	cccgagaacc	acaggtgtac	accctgcccc	420
catcccggga	ttagctgacc	aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	480
atccaagcga	catcgccgtg	gagtggaga	gcaatggca	gccggagaac	aactacaaga	540
ccacgcctcc	cgtgctggac	tccgacggct	ccttcttcct	ctacagcaag	ctcaccgtgg	600
acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	660
acaaccacta	cacgcagaag	agcctctccc	tgtctccggg	taaatgagtg	cgacggccgc	720
gactctagag	gat					733

<210> 82
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<221> misc_structure
<223> membrane proximal motif of class 1 cytokine receptors

<220>
<221> misc_feature
<222> (3)
<223> Xaa equals any

<400> 82
Trp Ser Xaa Trp Ser
1 5

<210> 83
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma activation site (GAS) containing promoter element

<400> 83	gcgccctcgag	atttccccga	aatctagatt	tcccccgaat	gatttccccg	aaatgatttc	60
	cccgaaatat	ctgccatctc	aattag				86

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<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> reverse primer useful for generation of a synthetic gamma
activation site (GAS) containing promoter element

<400> 84
gcggcaagct ttttgcaaag ccttaggc 27

<210> 85
<211> 271
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic GAS-SV40 promoter sequence

<400> 85
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttcccg 60
aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc
gcccttaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 120
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagttagt gaggaggctt 180
tttggaggc ctaggcttt gcaaaaagct t 240
271

<210> 86
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 86
gcgctcgagg gatgacagcgt atagaacccc gg 32

<210> 87
<211> 31
<212> DNA
<213> Artificial Sequence

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<220>
<221> primer_bind
<223> primer useful for generation of a EGR/SEAP reporter construct

<400> 87
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 88
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_binding
<223> NF-KB binding site

<400> 88
ggggactttc cc 12

<210> 89
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<223> forward primer useful for generation of a vector containing the
NF-KB promoter element

<400> 89
gcggcctcgaa ggggactttc ccggggactt tccggggact ttccggact ttccatcctg 60
ccatctcaat tag 73

<210> 90
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<223> Synthetic NF-KB/SV40 promoter

<400> 90
ctcgaggggaa ctttccccggg gactttccgg ggactttccg ggactttcca tctgccatct 60
caatttagtca gcaaccatag tcccgcctt aactccgccc atcccgcccc taactccgccc 120
cagttccgccc cattctccgc cccatggctg actaattttt tttatattatg cagaggccga 180

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ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttg gaggcctagg 240
ctttgcaaa aagctt 256